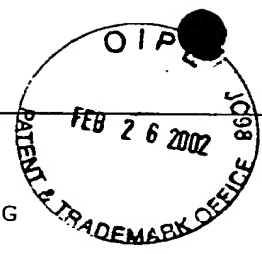


#7



#7

1

SEQUENCE LISTING

<110> Norbert Schweifer
Marwa Scherl-Mostageer
Wolfgang Sommergruber
Roger Abseher

<120> Tumorassoziiertes Antigen (B345)

<130> 0652.2280001

<140> US/09/899,569

<141> 2001-07-06

<150> DE 100 33 080.0

<151> 2000-07-07

<150> DE 101 19 294.0

<151> 2001-04-19

<150> US 60/243,158

<151> 2000-10-25

<150> US 60/297,747

<151> 2001-06-14

<160> 40

<170> PatentIn Ver. 2.1

<210> 1

<211> 5897

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (5348)...(5348)

<223> n is any nucleotide of a, t, g or c

<220>

<221> misc_feature

<222> (5360)...(5360)

<223> n is any nucleotide of a, t, g or c

<220>

<221> misc_feature

<222> (5425)...(5425)

<223> n is any nucleotide of a, t, g or c

<220>

<221> misc_feature

<222> (5438)...(5438)

<223> n is any nucleotide of a, t, g or c

<220>

<221> 5'UTR

A1

<222> (1)..(214)

<220>

<221> CDS

<222> (215)..(2464)

<220>

<221> 3'UTR

<222> (2465)..(5897)

<400> 1

cttgagatat tagaattcgc gactcctgaa ctgcgggggc tctatcgcac tgctaggggt 60

tctgctgctg ggtgcggcgc gcctgccgcg cggggcagaa gcttttgaga ttgctctgcc 120

acgagaaaagc aacattacag ttctcataaa gctgggggacc ccgactctgc tggcaaaacc 180

ctgttacatc gtcatttcta aaagacatat aacc atg ttg tcc atc aag tct gga 235

Met Leu Ser Ile Lys Ser Gly

1

5

gaa aga ata gtc ttt acc ttt agc tgc cag agt cct gag aat cac ttt 283

Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser Pro Glu Asn His Phe

10

15

20

gtc ata gag atc cag aaa aat att gac tgt atg tca ggc cca tgt cct 331

Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met Ser Gly Pro Cys Pro

25

30

35

ttt ggg gag gtt cag ctt cag ccc tcg aca tcg ttg ttg cct acc ctc 379

Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser Leu Leu Pro Thr Leu

40

45

50

55

aac aga act ttc atc tgg gat gtc aaa gct cat aag agc atc ggt tta 427

Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His Lys Ser Ile Gly Leu

60

65

70

gag ctg cag ttt tcc atc cct cgc ctg agg cag atc ggt ccg ggt gag 475

Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln Ile Gly Pro Gly Glu

75

80

85

agc tgc cca gac gga gtc act cac tcc atc agc ggc cga atc gat gcc 523

Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser Gly Arg Ile Asp Ala

90

95

100

acc gtg gtc agg atc gga acc ttc tgc agc aat ggc act gtg tcc cgg 571

Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg

105

110

115

atc aag atg caa gaa gga gtg aaa atg gcc tta cac ctc cca tgg ttc 619

Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu His Leu Pro Trp Phe

120

125

130

135

cac ccc aga aat gtc tcc ggc ttc agc att gca aac cgc tca tct ata 667
 His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala Asn Arg Ser Ser Ile
 140 145 150

aaa cgt ctg tgc atc atc gag tct gtg ttt gag ggt gaa ggc tca gca 715
 Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu Gly Glu Gly Ser Ala
 155 160 165

acc ctg atg tct gcc aac tac cca gaa ggc ttc cct gag gat gag ctc 763
 Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe Pro Glu Asp Glu Leu
 170 175 180

atg acg tgg cag ttt gtc gtt cct gca cac ctg cgg gcc agc gtc tcc 811
 Met Thr Trp Gln Phe Val Val Pro Ala His Leu Arg Ala Ser Val Ser
 185 190 195

ttc ctc aac ttc aac ctc tcc aac tgt gag agg aag gag gag cgg gtt 859
 Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg Lys Glu Glu Arg Val
 200 205 210 215

gag tac tac atc ccg ggc tcc acc acc aac ccc gag gtg ttc aag ctg 907
 Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys Leu
 220 225 230

gag gac aag cag cct ggg aac atg gcg ggg aac ttc aac ctc tct ctg 955
 Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu
 235 240 245

caa ggc tgt gac caa gat gcc caa agt cca ggg atc ctc cgg ctg cag 1003
 Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg Leu Gln
 250 255 260

ttc caa gtt ttg gtc caa cat cca caa aat gaa agc aat aaa atc tac 1051
 Phe Gln Val Leu Val Gln His Pro Gln Asn Glu Ser Asn Lys Ile Tyr
 265 270 275

gtg gtt gac ttg agt aat gag cga gcc atg tca ctc acc atc gag cca 1099
 Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser Leu Thr Ile Glu Pro
 280 285 290 295

cgg ccc gtc aaa cag agc cgc aag ttt gtc cct ggc tgt ttc gtg tgt 1147
 Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro Gly Cys Phe Val Cys
 300 305 310

cta gaa tct cgg acc tgc agt agc aac ctc acc ctg aca tct ggc tcc 1195
 Leu Glu Ser Arg Thr Cys Ser Ser Asn Leu Thr Leu Thr Ser Gly Ser
 315 320 325

aaa cac aaa atc tcc ttc ctt tgt gat gat ctg aca cgt ctg tgg atg 1243
 Lys His Lys Ile Ser Phe Leu Cys Asp Asp Leu Thr Arg Leu Trp Met
 330 335 340

aat gtg gaa aaa acc ata agc tgc aca gac cac cgg tac tgc caa agg 1291

Asn	Val	Glu	Lys	Thr	Ile	Ser	Cys	Thr	Asp	His	Arg	Tyr	Cys	Gln	Arg		
345						350					355						
aaa	tcc	tac	tca	ctc	cag	gtg	ccc	agt	gac	atc	ctc	cac	ctg	cct	gtg	1339	
Lys	Ser	Tyr	Ser	Leu	Gln	Val	Pro	Ser	Asp	Ile	Leu	His	Leu	Pro	Val		
360					365					370					375		
gag	ctg	cat	gac	ttc	tcc	tgg	aag	ctg	ctg	gtg	ccc	aag	gac	agg	ctc	1387	
Glu	Leu	His	Asp	Phe	Ser	Trp	Lys	Leu	Leu	Val	Pro	Lys	Asp	Arg	Leu		
				380						385					390		
agc	ctg	gtg	ctg	gtg	cca	gcc	cag	aag	ctg	cag	cag	cat	aca	cac	gag	1435	
Ser	Leu	Val	Leu	Val	Pro	Ala	Gln	Lys	Leu	Gln	Gln	His	Thr	His	Glu		
				395				400						405			
aag	ccc	tgc	aac	acc	agc	ttc	agc	tac	ctc	gtg	gcc	agt	gcc	ata	ccc	1483	
Lys	Pro	Cys	Asn	Thr	Ser	Phe	Ser	Tyr	Leu	Val	Ala	Ser	Ala	Ile	Pro		
		410					415						420				
agc	cag	gac	ctg	tac	ttc	ggc	tcc	ttc	tgc	ccg	gga	ggc	tct	atc	aag	1531	
Ser	Gln	Asp	Leu	Tyr	Phe	Gly	Ser	Phe	Cys	Pro	Gly	Gly	Ser	Ile	Lys		
		425				430						435					
cag	atc	cag	gtg	aag	cag	aac	atc	tcg	gtg	acc	ctt	cgc	acc	ttt	gcc	1579	
Gln	Ile	Gln	Val	Lys	Gln	Asn	Ile	Ser	Val	Thr	Leu	Arg	Thr	Phe	Ala		
440					445					450					455		
ccc	agc	ttc	caa	caa	gag	gcc	tcc	agg	cag	ggt	ctg	acg	gtg	tcc	ttt	1627	
Pro	Ser	Phe	Gln	Gln	Glu	Ala	Ser	Arg	Gln	Gly	Leu	Thr	Val	Ser	Phe		
				460					465						470		
ata	cct	tat	ttc	aaa	gag	gaa	ggc	gtt	ttc	acg	gtg	acc	cct	gac	aca	1675	
Ile	Pro	Tyr	Phe	Lys	Glu	Glu	Gly	Val	Phe	Thr	Val	Thr	Pro	Asp	Thr		
				475				480						485			
aaa	agc	aag	gtc	tac	ctg	agg	acc	ccc	aac	tgg	gac	cgg	ggc	ctg	cca	1723	
Lys	Ser	Lys	Val	Tyr	Leu	Arg	Thr	Pro	Asn	Trp	Asp	Arg	Gly	Leu	Pro		
		490					495					500					
tcc	ctc	acc	tct	gtg	tcc	tgg	aac	atc	agc	gtg	ccc	aga	gac	cag	gtg	1771	
Ser	Leu	Thr	Ser	Val	Ser	Trp	Asn	Ile	Ser	Val	Pro	Arg	Asp	Gln	Val		
		505				510					515						
gcc	tgc	ctg	act	ttc	ttt	aag	gag	cgg	agc	ggc	gtg	gtc	tgc	cag	aca	1819	
Ala	Cys	Leu	Thr	Phe	Phe	Lys	Glu	Arg	Ser	Gly	Val	Val	Cys	Gln	Thr		
520					525					530					535		
ggg	cgc	gca	ttc	atg	atc	atc	cag	gag	cag	cgg	acc	cgg	gct	gag	gag	1867	
Gly	Arg	Ala	Phe	Met	Ile	Ile	Gln	Glu	Gln	Arg	Thr	Arg	Ala	Glu	Glu		
				540					545					550			
atc	ttc	agc	ctg	gac	gag	gat	gtg	ctc	ccc	aag	cca	agc	ttc	cac	cat	1915	
Ile	Phe	Ser	Leu	Asp	Glu	Asp	Val	Leu	Pro	Lys	Pro	Ser	Phe	His	His		
			555					560						565			
cac	agc	ttc	tgg	gtc	aac	atc	tct	aac	tgc	agc	ccc	acg	agc	ggc	aag	1963	

A

atgacagctc atgtgctcct caacttaggc tgtgcggtta gccagcctgt aatgagagga 2794
 gagaggcctg agtcacctag cataggggtg cagcaagccc tggattcaga gtgttaaaca 2854
 gaggcttgcc ctcttcagga caacagttcc aattccaagg agcctacctg aggtccctac 2914
 tctcactggg gtccccagga tgaaaacgac aatgtgcctt tttattatta tttatttggg 2974
 ggtcctgtgt tatttaagag atcaaagtga taaccaccta gctcttttca cctgacttag 3034
 taataactca tactaactgg tttggatgcc tgggttgtga cttctactga ccgctagata 3094
 aacgtgtgcc tgtccccag gtggtgggaa taatttaca tctgtccaac cagaaaagaa 3154
 tgtgtgtgtt tgagcagcat tgacacatat ctgctttgat aagagacttc ctgattctct 3214
 aggtcggttc gtggttatcc cattgtggaa attcatcttg aatcccattg tcctatagtc 3274
 ctagcaataa gagaaatttc ctcaagtttc catgtgcggt tctcctagct gcagcaatac 3334
 tttgacattt aaagagaaat ttagagaata ttctcatcct ctaaaaatgt ttaaataatat 3394
 accaaacagt ggccccctgc attagttttc tgttgccact gcaaccatt acttggttagc 3454
 ttaaaaacaa cacattagct tatagtcttg gggatcagaa ttccaaaatg gatgtccctg 3514
 aatgaaaatc aaggtgtcag cagagctgtg ctcttctga aggctctagg gagaagccgg 3574
 ttcttgcca tttcaagctt ctagaggctg gctgcattcc caggctccag tggctggtca 3634
 agcttttctc acatggcatc actgtgacac tggccctccc acttccctct ttgacttaca 3694
 aagcccacca ggaagatcca ggataatctc tccatctaaa gatccttcat catcctggaa 3754
 gagccttttg ccatgcaaga caacatagcc acagggtggg attaggacca ggacatcttt 3814
 ggggtgctgt tattctgcct accacacctt cctgccacbg actccacag gagaggctac 3874
 aaaatgatct ggcgcacagg gatgttttgt ttagcttgcg gactctaaca cttaaaaaaa 3934
 cccagatca gaagatctgg ccatgctggg gctcacattc tcacctagca acaactggct 3994
 ggagctgggc accagctctg cttttagaag ggggtgtccac ttcaccagg caccacagcc 4054
 cacactacgc cctatcactt cccacaatga ggctaagtgt ttgtttctac tgatcaatgc 4114
 ccctgcagg tgcatttatt gtaatgaaaa agaaagactg ggattaatct ctaatcagg 4174
 gagtagacca tgagaccaat gtgtgctcac attacccttt ttcttttttt tctttttctt 4234
 tttctttttt tttttaatgt gagacaggat ctcatctgt tgcctaggct ggagtgcagt 4294
 ggcgcaatct cggctcactg caacctctgc ctctgggct caagcaattc tcccacctca 4354
 gcctcccaa tagctgggat cactggcaca aaccaccatg cccagctaatt tttgtatttt 4414
 ttgtagagac agggtttcac catgttgccc aggtgtgtct caacctcctg ggctcaagca 4474

atcctcctgc ctcggcctcc caaagtgctg ggattacaga tgtgagccac cgcattccagc 4534
 cccacaccct catttatacc aattacctgc ccagtaactg tggacttttg cttcctcacc 4594
 cctgctctga tctggaagga gagggattat gttatagctt gtcagcacag tccaagttc 4654
 aatattttctg cggcaaaaac ttccttcaaa aaataaatgt acttcattgt attcaatgaa 4714
 ttcaccttgg aaatgcaccg cctcaacttg ttcacatggc ataaatgaaa ggaattttat 4774
 agtctcctaa atggcgtgta ctgcaagacc tcttgaacac tttccagagg ataggatatt 4834
 taagtcatgc ccttggcggt gcctatggca cctttccctt ctgaaagtct ggttcctgcc 4894
 cagtgcacct tggccttgtg agccgagatg ctgaccctgc ataaagggcc aaaggagggc 4954
 tgcggcttcc ttcctcact gaagagccct tatttgaatt cactgtgtgg agccctagcc 5014
 ctccattctc gacattcccc aacctcccag ccccttccaa gcaggactag gtgccctgca 5074
 ttccacccaa ggtgggattg gccttcctta ggctggctac ttgtcaccat caccgacatc 5134
 actgttgctt gcaaggacac cacgtggcca ttttcttca actgagggct caaaactcct 5194
 ggacaagttg ctggctcctg agaccagtat ttcttgagm tgtgcctcag tgaaggggcc 5254
 cagcctgagg aacctgggt cttttcttta aagcccaggc cccacttaca taaaacattt 5314
 cagggtcact ggaaacagtg aagtgccatt tgtngaagcc tactgnatgc cagccctactg 5374
 ctcatccacg tggatgccca tgcctacgag gaaggccagc gcatgcagga ntgggtctcta 5434
 atgntgtggt cattgcacag aagggaaagg tctcaaggaa gagtcaactg ggacaagcac 5494
 aagcccaccg gacatggcct tggtaaaggt tagcagactg gtgtgtgtgg atctgcagtg 5554
 cttcactgga aataatttat tcattgcaga tacttttttag gtggcatttt attcatttcc 5614
 tgtgctttta ataaacaaat gtaccaaaaa acaagtatca agctgtttta gtgcttcggc 5674
 tacttgctcc ctggttcagt agaggccccg gtttccagct tgttgactgt gacaggctca 5734
 gcatgggctc agcagatgct gtcttaattt gtggatgata cagaaagcca ggctttggga 5794
 tacaagttct ttcctcttca tttgatgccg tgcactgtgt gaagcagatg ttttgtccg 5854
 gaaataaaaa taatagtctt ggagtctcgc caaaaaaaaa aag 5897

<210> 2
 <211> 749
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys
 1 5 10 15
 Gln Ser Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn Ile Asp
 20 25 30
 Cys Met Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln Pro Ser
 35 40 45
 Thr Ser Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp Val Lys
 50 55 60
 Ala His Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro Arg Leu
 65 70 75 80
 Arg Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr His Ser
 85 90 95
 Ile Ser Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr Phe Cys
 100 105 110
 Ser Asn Gly Thr Val Ser Arg Ile Lys Met Gln Glu Gly Val Lys Met
 115 120 125
 Ala Leu His Leu Pro Trp Phe His Pro Arg Asn Val Ser Gly Phe Ser
 130 135 140
 Ile Ala Asn Arg Ser Ser Ile Lys Arg Leu Cys Ile Ile Glu Ser Val
 145 150 155 160
 Phe Glu Gly Glu Gly Ser Ala Thr Leu Met Ser Ala Asn Tyr Pro Glu
 165 170 175
 Gly Phe Pro Glu Asp Glu Leu Met Thr Trp Gln Phe Val Val Pro Ala
 180 185 190
 His Leu Arg Ala Ser Val Ser Phe Leu Asn Phe Asn Leu Ser Asn Cys
 195 200 205
 Glu Arg Lys Glu Glu Arg Val Glu Tyr Tyr Ile Pro Gly Ser Thr Thr
 210 215 220
 Asn Pro Glu Val Phe Lys Leu Glu Asp Lys Gln Pro Gly Asn Met Ala
 225 230 235 240
 Gly Asn Phe Asn Leu Ser Leu Gln Gly Cys Asp Gln Asp Ala Gln Ser
 245 250 255
 Pro Gly Ile Leu Arg Leu Gln Phe Gln Val Leu Val Gln His Pro Gln
 260 265 270
 Asn Glu Ser Asn Lys Ile Tyr Val Val Asp Leu Ser Asn Glu Arg Ala
 275 280 285
 Met Ser Leu Thr Ile Glu Pro Arg Pro Val Lys Gln Ser Arg Lys Phe
 290 295 300

Val Pro Gly Cys Phe Val Cys Leu Glu Ser Arg Thr Cys Ser Ser Asn
 305 310 315 320
 Leu Thr Leu Thr Ser Gly Ser Lys His Lys Ile Ser Phe Leu Cys Asp
 325 330 335
 Asp Leu Thr Arg Leu Trp Met Asn Val Glu Lys Thr Ile Ser Cys Thr
 340 345 350
 Asp His Arg Tyr Cys Gln Arg Lys Ser Tyr Ser Leu Gln Val Pro Ser
 355 360 365
 Asp Ile Leu His Leu Pro Val Glu Leu His Asp Phe Ser Trp Lys Leu
 370 375 380
 Leu Val Pro Lys Asp Arg Leu Ser Leu Val Leu Val Pro Ala Gln Lys
 385 390 395 400
 Leu Gln Gln His Thr His Glu Lys Pro Cys Asn Thr Ser Phe Ser Tyr
 405 410 415
 Leu Val Ala Ser Ala Ile Pro Ser Gln Asp Leu Tyr Phe Gly Ser Phe
 420 425 430
 Cys Pro Gly Gly Ser Ile Lys Gln Ile Gln Val Lys Gln Asn Ile Ser
 435 440 445
 Val Thr Leu Arg Thr Phe Ala Pro Ser Phe Gln Gln Glu Ala Ser Arg
 450 455 460
 Gln Gly Leu Thr Val Ser Phe Ile Pro Tyr Phe Lys Glu Glu Gly Val
 465 470 475 480
 Phe Thr Val Thr Pro Asp Thr Lys Ser Lys Val Tyr Leu Arg Thr Pro
 485 490 495
 Asn Trp Asp Arg Gly Leu Pro Ser Leu Thr Ser Val Ser Trp Asn Ile
 500 505 510
 Ser Val Pro Arg Asp Gln Val Ala Cys Leu Thr Phe Phe Lys Glu Arg
 515 520 525
 Ser Gly Val Val Cys Gln Thr Gly Arg Ala Phe Met Ile Ile Gln Glu
 530 535 540
 Gln Arg Thr Arg Ala Glu Glu Ile Phe Ser Leu Asp Glu Asp Val Leu
 545 550 555 560
 Pro Lys Pro Ser Phe His His His Ser Phe Trp Val Asn Ile Ser Asn
 565 570 575
 Cys Ser Pro Thr Ser Gly Lys Gln Leu Asp Leu Leu Phe Ser Val Thr
 580 585 590
 Leu Thr Pro Arg Thr Val Asp Leu Thr Val Ile Leu Ile Ala Ala Val
 595 600 605

Gly Gly Gly Val Leu Leu Leu Ser Ala Leu Gly Leu Ile Ile Cys Cys
 610 615 620
 Val Lys Lys Lys Lys Lys Lys Thr Asn Lys Gly Pro Ala Val Gly Ile
 625 630 635 640
 Tyr Asn Gly Asn Ile Asn Thr Glu Met Pro Gly Ser Gln Lys Ser Phe
 645 650 655
 Arg Lys Gly Glu Arg Thr Met Thr Pro Met Cys Met Gln Ser Ser Arg
 660 665 670
 Thr Pro Trp Tyr Met Gly Ile Cys Tyr Arg Ile Pro Ala Ala Pro Ser
 675 680 685
 Cys Ser Gln Arg Trp Thr Pro Thr Gly Arg Ser Arg Ala Pro Trp Gly
 690 695 700
 Ser Val Leu Pro Pro His Pro Pro Tyr Ala Pro Gly Pro Gln Leu Gln
 705 710 715 720
 Ser Trp Pro Leu Arg Ser His Leu Leu Ala Pro Leu Leu Ser Leu Arg
 725 730 735
 Val Asn Arg Thr Pro Ser Pro Ile Pro Thr Met Gly Met
 740 745

<210> 3
 <211> 6163
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> (1)..(282)

<220>
 <221> GC_signal
 <222> (147)..(157)

<220>
 <221> misc_feature
 <222> (201)..(209)
 <223> cap signal; Transcription start

<220>
 <221> 3'UTR
 <222> (2794)..(6163)

<220>
 <221> 3'UTR
 <222> (2794)..(6163)

<220>
 <221> CDS

<222> (283)..(2793)

<400> 3

ccaacgccgc aatggggagt agtagggacc cagcaacccg gtgccgggag ccctgcaccc 60
 tgggagggag aggcggtcgc tgaggcagga agaggaggag gagagagagg agggacgcac 120
 cgggtcagct cgcgacccctg ctgcgcaggg cggggctcgg gccgggtccgc ccgcgcgcag 180
 gtgagtgagc cagggcggag cgcagctgcg ccgggcttgg gcgcctgggg ccgccgctcc 240
 ccaccgtcgt tttccccacc gaggccgagg cgtcccggag tc atg gcc ggc ctg 294
 Met Ala Gly Leu

1

aac tgc ggg gtc tct atc gca ctg cta ggg gtt ctg ctg ctg ggt gcg 342
 Asn Cys Gly Val Ser Ile Ala Leu Leu Gly Val Leu Leu Leu Gly Ala
 5 10 15 20

gcg cgc ctg ccg cgc ggg gca gaa gct ttt gag att gct ctg cca cga 390
 Ala Arg Leu Pro Arg Gly Ala Glu Ala Phe Glu Ile Ala Leu Pro Arg
 25 30 35

gaa agc aac att aca gtt ctc ata aag ctg ggg acc ccg act ctg ctg 438
 Glu Ser Asn Ile Thr Val Leu Ile Lys Leu Gly Thr Pro Thr Leu Leu
 40 45 50

gca aaa ccc tgt tac atc gtc att tct aaa aga cat ata acc atg ttg 486
 Ala Lys Pro Cys Tyr Ile Val Ile Ser Lys Arg His Ile Thr Met Leu
 55 60 65

tcc atc aag tct gga gaa aga ata gtc ttt acc ttt agc tgc cag agt 534
 Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser
 70 75 80

cct gag aat cac ttt gtc ata gag atc cag aaa aat att gac tgt atg 582
 Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met
 85 90 95 100

tca ggc cca tgt cct ttt ggg gag gtt cag ctt cag ccc tcg aca tcg 630
 Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser
 105 110 115

ttg ttg cct acc ctc aac aga act ttc atc tgg gat gtc aaa gct cat 678
 Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His
 120 125 130

aag agc atc ggt tta gag ctg cag ttt tcc atc cct cgc ctg agg cag 726
 Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln
 135 140 145

atc ggt ccg ggt gag agc tgc cca gac gga gtc act cac tcc atc agc 774
 Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser
 150 155 160

ggc cga atc gat gcc acc gtg gtc agg atc gga acc ttc tgc agc aat 822
 Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn

165	170	175	180	
ggc act gtg tcc cgg atc aag atg caa gaa gga gtg aaa atg gcc tta				870
Gly Thr Val Ser Arg Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu				
	185	190	195	
cac ctc cca tgg ttc cac ccc aga aat gtc tcc ggc ttc agc att gca				918
His Leu Pro Trp Phe His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala				
	200	205	210	
aac cgc tca tct ata aaa cgt ctg tgc atc atc gag tct gtg ttt gag				966
Asn Arg Ser Ser Ile Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu				
	215	220	225	
ggt gaa ggc tca gca acc ctg atg tct gcc aac tac cca gaa ggc ttc				1014
Gly Glu Gly Ser Ala Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe				
	230	235	240	
cct gag gat gag ctc atg acg tgg cag ttt gtc gtt cct gca cac ctg				1062
Pro Glu Asp Glu Leu Met Thr Trp Gln Phe Val Val Pro Ala His Leu				
	245	250	255	260
cgg gcc agc gtc tcc ttc ctc aac ttc aac ctc tcc aac tgt gag agg				1110
Arg Ala Ser Val Ser Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg				
	265	270	275	
aag gag gag cgg gtt gaa tac tac atc ccg ggc tcc acc acc aac ccc				1158
Lys Glu Glu Arg Val Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro				
	280	285	290	
gag gtg ttc aag ctg gag gac aag cag cct ggg aac atg gcg ggg aac				1206
Glu Val Phe Lys Leu Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn				
	295	300	305	
ttc aac ctc tct ctg caa ggc tgt gac caa gat gcc caa agt cca ggg				1254
Phe Asn Leu Ser Leu Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly				
	310	315	320	
atc ctc cgg ctg cag ttc caa gtt ttg gtc caa cat cca caa aat gaa				1302
Ile Leu Arg Leu Gln Phe Gln Val Leu Val Gln His Pro Gln Asn Glu				
	325	330	335	340
agc aat aaa atc tac gtg gtt gac ttg agt aat gag cga gcc atg tca				1350
Ser Asn Lys Ile Tyr Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser				
	345	350	355	
ctc acc atc gag cca cgg ccc gtc aaa cag agc cgc aag ttt gtc cct				1398
Leu Thr Ile Glu Pro Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro				
	360	365	370	
ggc tgt ttc gtg tgt cta gaa tct cgg acc tgc agt agc aac ctc acc				1446
Gly Cys Phe Val Cys Leu Glu Ser Arg Thr Cys Ser Ser Asn Leu Thr				
	375	380	385	
ctg aca tct ggc tcc aaa cac aaa atc tcc ttc ctt tgt gat gat ctg				1494

A1

Leu	Thr	Ser	Gly	Ser	Lys	His	Lys	Ile	Ser	Phe	Leu	Cys	Asp	Asp	Leu	
390						395					400					
aca	cgt	ctg	tgg	atg	aat	gtg	gaa	aaa	acc	ata	agc	tgc	aca	gac	cac	1542
Thr	Arg	Leu	Trp	Met	Asn	Val	Glu	Lys	Thr	Ile	Ser	Cys	Thr	Asp	His	
405					410				415						420	
cgg	tac	tgc	caa	agg	aaa	tcc	tac	tca	ctc	cag	gtg	ccc	agt	gac	atc	1590
Arg	Tyr	Cys	Gln	Arg	Lys	Ser	Tyr	Ser	Leu	Gln	Val	Pro	Ser	Asp	Ile	
			425						430					435		
ctc	cac	ctg	cct	gtg	gag	ctg	cat	gac	ttc	tcc	tgg	aag	ctg	ctg	gtg	1638
Leu	His	Leu	Pro	Val	Glu	Leu	His	Asp	Phe	Ser	Trp	Lys	Leu	Leu	Val	
			440					445						450		
ccc	aag	gac	agg	ctc	agc	ctg	gtg	ctg	gtg	cca	gcc	cag	aag	ctg	cag	1686
Pro	Lys	Asp	Arg	Leu	Ser	Leu	Val	Leu	Val	Pro	Ala	Gln	Lys	Leu	Gln	
		455					460					465				
cag	cat	aca	cac	gag	aag	ccc	tgc	aac	acc	agc	ttc	agc	tac	ctc	gtg	1734
Gln	His	Thr	His	Glu	Lys	Pro	Cys	Asn	Thr	Ser	Phe	Ser	Tyr	Leu	Val	
	470					475					480					
gcc	agt	gcc	ata	ccc	agc	cag	gac	ctg	tac	ttc	ggc	tcc	ttc	tgc	ccg	1782
Ala	Ser	Ala	Ile	Pro	Ser	Gln	Asp	Leu	Tyr	Phe	Gly	Ser	Phe	Cys	Pro	
485					490					495					500	
gga	ggc	tct	atc	aag	cag	atc	cag	gtg	aag	cag	aac	atc	tgc	gtg	acc	1830
Gly	Gly	Ser	Ile	Lys	Gln	Ile	Gln	Val	Lys	Gln	Asn	Ile	Ser	Val	Thr	
				505					510					515		
ctt	cgc	acc	ttt	gcc	ccc	agc	ttc	caa	caa	gag	gcc	tcc	agg	cag	ggc	1878
Leu	Arg	Thr	Phe	Ala	Pro	Ser	Phe	Gln	Gln	Glu	Ala	Ser	Arg	Gln	Gly	
			520					525					530			
ctg	acg	gtg	tcc	ttt	ata	cct	tat	ttc	aaa	gag	gaa	ggc	gtt	ttc	acg	1926
Leu	Thr	Val	Ser	Phe	Ile	Pro	Tyr	Phe	Lys	Glu	Glu	Gly	Val	Phe	Thr	
			535				540					545				
gtg	acc	cct	gac	aca	aaa	agc	aag	gtc	tac	ctg	agg	acc	ccc	aac	tgg	1974
Val	Thr	Pro	Asp	Thr	Lys	Ser	Lys	Val	Tyr	Leu	Arg	Thr	Pro	Asn	Trp	
	550					555					560					
gac	cgg	ggc	ctg	cca	tcc	ctc	acc	tct	gtg	tcc	tgg	aac	atc	agc	gtg	2022
Asp	Arg	Gly	Leu	Pro	Ser	Leu	Thr	Ser	Val	Ser	Trp	Asn	Ile	Ser	Val	
565					570					575					580	
ccc	aga	gac	cag	gtg	gcc	tgc	ctg	act	ttc	ttt	aag	gag	cgg	agc	ggc	2070
Pro	Arg	Asp	Gln	Val	Ala	Cys	Leu	Thr	Phe	Phe	Lys	Glu	Arg	Ser	Gly	
			585						590					595		
gtg	gtc	tgc	cag	aca	ggg	cgc	gca	ttc	atg	atc	atc	cag	gag	cag	cgg	2118
Val	Val	Cys	Gln	Thr	Gly	Arg	Ala	Phe	Met	Ile	Ile	Gln	Glu	Gln	Arg	
			600					605					610			

A1

acc cgg gct gag gag atc ttc agc ctg gac gag gat gtg ctc ccc aag 2166
 Thr Arg Ala Glu Glu Ile Phe Ser Leu Asp Glu Asp Val Leu Pro Lys
 615 620 625

cca agc ttc cac cat cac agc ttc tgg gtc aac atc tct aac tgc agc 2214
 Pro Ser Phe His His His Ser Phe Trp Val Asn Ile Ser Asn Cys Ser
 630 635 640

ccc acg agc ggc aag cag cta gac ctg ctc ttc tcg gtg aca ctt acc 2262
 Pro Thr Ser Gly Lys Gln Leu Asp Leu Leu Phe Ser Val Thr Leu Thr
 645 650 655 660

cca agg act gtg gac ttg act gtc atc ctc atc gca gcg gtg gga ggt 2310
 Pro Arg Thr Val Asp Leu Thr Val Ile Leu Ile Ala Ala Val Gly Gly
 665 670 675

gga gtc tta ctg ctg tct gcc ctc ggg ctc atc att tgc tgt gtg aaa 2358
 Gly Val Leu Leu Leu Ser Ala Leu Gly Leu Ile Ile Cys Cys Val Lys
 680 685 690

aag aag aaa aag aag aca aac aag ggc ccc gct gtg ggt atc tac aat 2406
 Lys Lys Lys Lys Lys Thr Asn Lys Gly Pro Ala Val Gly Ile Tyr Asn
 695 700 705

ggc aac atc aat act gag atg ccg agg cag cca aaa aag ttt cag aaa 2454
 Gly Asn Ile Asn Thr Glu Met Pro Arg Gln Pro Lys Lys Phe Gln Lys
 710 715 720

ggg cga aag gac aat gac tcc cat gtg tat gca gtc atc gag gac acc 2502
 Gly Arg Lys Asp Asn Asp Ser His Val Tyr Ala Val Ile Glu Asp Thr
 725 730 735 740

atg gta tat ggg cat ctg cta cag gat tcc agc ggc tcc ttc ctg cag 2550
 Met Val Tyr Gly His Leu Leu Gln Asp Ser Ser Gly Ser Phe Leu Gln
 745 750 755

cca gag gtg gac acc tac cgg ccg ttc cag ggc acc atg ggg gtc tgt 2598
 Pro Glu Val Asp Thr Tyr Arg Pro Phe Gln Gly Thr Met Gly Val Cys
 760 765 770

cct ccc tcc cca ccc acc ata tgc tcc agg gcc cca act gca aag ttg 2646
 Pro Pro Ser Pro Pro Thr Ile Cys Ser Arg Ala Pro Thr Ala Lys Leu
 775 780 785

gcc act gag gag cca cct cct cgc tcc cct cct gag tct gag agt gaa 2694
 Ala Thr Glu Glu Pro Pro Pro Arg Ser Pro Pro Glu Ser Glu Ser Glu
 790 795 800

ccg tac acc ttc tcc cat ccc aac aat ggg gat gta agc agc aag gac 2742
 Pro Tyr Thr Phe Ser His Pro Asn Asn Gly Asp Val Ser Ser Lys Asp
 805 810 815 820

aca gac att ccc tta ctg aac act cag gag ccc atg gag cca gca gaa 2790
 Thr Asp Ile Pro Leu Leu Asn Thr Gln Glu Pro Met Glu Pro Ala Glu
 825 830 835

taa cttgatccat tccagacgct ttgctgagtt tcataaagca gggcactgag 2843
 acaccggtcc gtgttcctaa ccagaaatcc taaagaagag gaattataca gaaggaacag 2903
 caggaggttt tcctggacac cgccaacttc acattgctca gtggactcat tctaaggcca 2963
 agacattgaa aatgatgaat tccaatctgg atacagtcac gacagctcat gtgctcctca 3023
 acttaggctg tgcggttagc cagcctgtaa tgagaggaga gaggcctgag tcacctagca 3083
 tagggttgca gcaagccctg gattcagagt gttaaacaga ggcttgcctt cttcaggaca 3143
 acagttccaa ttccaaggag cctacctgag gtccctactc tcaactgggt cccaggatg 3203
 aaaacgacaa tgtgcctttt tattattatt tatttgggtg tcctgtgtta tttaagagat 3263
 caaatgtata accacctagc tcttttcacc tgacttagta ataactcata ctaactgggt 3323
 tggatgcctg ggttgtgact tctactgacc gctagataaa cgtgtgcctg tccccaggt 3383
 A1 ggtggaata atttacaatc tgtccaacca gaaaagaatg tgtgtgtttg agcagcattg 3443
 acacatatct gctttgataa gagacttctt gattctctag gtgggttcgt ggttatccca 3503
 ttgtggaaat tcatcttgaa tccattgtc ctatagtcct agcaataaga gaaatttctt 3563
 caagtttcca tgtgcggttc tcctagctgc agcaatactt tgacatttaa agagaaattt 3623
 agagaatatt ctcatcctct aaaaatgttt aaatatatac caaacagtgg cccctgcat 3683
 tagttttctg ttgccactgc aaccattac ttggtagctt aaaaacaaca cattagctta 3743
 tagtctggg gatcagaatt ccaaatgga tgtccctgaa tgaaatcaa ggtgtcagca 3803
 gagctgtgct ccttctgaag gctctagga gaagccggt ccttgccatt tcaagcttct 3863
 agaggctggc tgcattccca ggctccagt gctgggtcaag cttttctcac atggcatcac 3923
 tgtgacactg gccctccac ttccctcttt gacttacaaa gccaccagg aagatccagg 3983
 ataatctctc catctaaaga tccttcatca tcctggaaga gccttttgcc atgcaagaca 4043
 acatagccac aggtggggat taggaccagg acatctttgg ggtgctgtta ttctgcctac 4103
 cacaccttc tgccactgac tcccacagga gaggtacaa aatgatctgg cgcacaggga 4163
 tgttttgttt agcttgcgga ctctaact taaaaaacc ccagatcaga agatctggcc 4223
 atgtggggc tcacattctc acctagcaac aactggctgg agctgggcac cagctctgcc 4283
 tttagaagg gtgtccactt caccaggtca ccacagcca cactacgcc tatcatttc 4343
 cacaatgagg ctaagtgtt gtttctactg atcaatgcc ctgcagggtt catttattgt 4403
 aatgaaaaag aaagactggg attaattctt aatcagggtg gtagaccatg agaccaatgt 4463

gtgctcacat tacccttttt cttttttttt tttttctttt tctttttttt tttaatgtga 4523
 gacaggatct cattctgttg cctaggctgg agtgagtggt cgcaatctcg gctcactgca 4583
 acctctgcct cctgggctca agcaattctc ccacctcagc ctcccaaata gctgggatca 4643
 ctggcacaaa ccaccatgcc cagctaattt tgtatttttt gtagagacag ggtttcacca 4703
 tgttgcccag gctggtctca acctcctggg ctcaagcaat cctcctgcct cggcctccca 4763
 aagtgtggg attacagatg tgagccaccg catccagccc cacaccctca tttataccaa 4823
 ttacctgccc agtaactgtg gacttttgtt tcttcacccc tgctctgatc tggaaggaga 4883
 gggattatgt tatagcttgt cagcacagtc ccaagttcaa tatttctgcg gcaaaaactt 4943
 ccttcaaaaa ataatgttac ttcatgtat tcaatgaatt caccttgga atgcaccgcc 5003
 tcaacttggt cacatggcat aaatgaaagg aattttatag tctcctaaat ggctgtgact 5063
 gcaagacctt ttgaacactt tccagaggat aggatattta agtcatgccc ttggcgttgc 5123
 ctatggcacc tttcccttct gaaagtctgg ttcttgccca gtgacccttg gccttgtgag 5183
 ccgagatgct gaccctgcat aaagggccaa aggagggtg cggcttcctt ccctcactga 5243
 agagccctta tttgaattca ctgtgtggag ccctagccct ccattctcga cattcccaa 5303
 cctcccagcc ccttccaagc aggactaggt gccctgcatt ccaccaagg tgggattggc 5363
 cttccttagg ctggctactt gtcaccatca ccgacatcac tgttgctgc aaggacacca 5423
 cgtggccatt ttcttcaac tgagggtca aaactcctgg acaagttgct ggctcctgag 5483
 accagtattt cctggagctg tgcctcagtg aaggggccc gcctgaggaa ccctggctct 5543
 tttctttaa gcccaggccc cacttacata aaacatttca gggcactgg aaacagtga 5603
 gtgccatttg ttgaagccta ctgcatgcca gccactgct catccacgtg gtctgccatg 5663
 cctacgagga aggccagcgc atgcaggact ggtctcta at gctgtggtca ttgcacagaa 5723
 gggaaaggct tcaaggaaga gtcaactggg acaagcaca gccaccgga catggccttg 5783
 gtaaagggtta gcagactggg gtgtgtggat ctgcagtgct tcaactggaaa taatttatc 5843
 attgcagata ctttttaggt ggcattttat tcatttcctg tgctttaa at aaacaaatgt 5903
 accaaaaaac aagtatcaag ctgtttaagt gcttcggcta cttgtcccct ggttcagtag 5963
 agggcccggt ttcccagttg ttgactgtga caggctcagc atgggctcag cagatgctgt 6023
 ctttaatttg ggatgataca gaaagccagg ctttgggata caagttctt cctcttcatt 6083
 tgatgccgtg cactgtgtga agcagatgtt tttgtccgga aataaaaaata atagtcttg 6143

A1

agtcctcgcca aaaaaaaaaa

6163

<210> 4
 <211> 836
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ala Gly Leu Asn Cys Gly Val Ser Ile Ala Leu Leu Gly Val Leu
 1 5 10 15
 Leu Leu Gly Ala Ala Arg Leu Pro Arg Gly Ala Glu Ala Phe Glu Ile
 20 25 30
 Ala Leu Pro Arg Glu Ser Asn Ile Thr Val Leu Ile Lys Leu Gly Thr
 35 40 45
 Pro Thr Leu Leu Ala Lys Pro Cys Tyr Ile Val Ile Ser Lys Arg His
 50 55 60
 Ile Thr Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe
 65 70 75 80
 Ser Cys Gln Ser Pro Glu Asn His Phe Val Ile Glu Ile Gln Lys Asn
 85 90 95
 Ile Asp Cys Met Ser Gly Pro Cys Pro Phe Gly Glu Val Gln Leu Gln
 100 105 110
 Pro Ser Thr Ser Leu Leu Pro Thr Leu Asn Arg Thr Phe Ile Trp Asp
 115 120 125
 Val Lys Ala His Lys Ser Ile Gly Leu Glu Leu Gln Phe Ser Ile Pro
 130 135 140
 Arg Leu Arg Gln Ile Gly Pro Gly Glu Ser Cys Pro Asp Gly Val Thr
 145 150 155 160
 His Ser Ile Ser Gly Arg Ile Asp Ala Thr Val Val Arg Ile Gly Thr
 165 170 175
 Phe Cys Ser Asn Gly Thr Val Ser Arg Ile Lys Met Gln Glu Gly Val
 180 185 190
 Lys Met Ala Leu His Leu Pro Trp Phe His Pro Arg Asn Val Ser Gly
 195 200 205
 Phe Ser Ile Ala Asn Arg Ser Ser Ile Lys Arg Leu Cys Ile Ile Glu
 210 215 220
 Ser Val Phe Glu Gly Glu Gly Ser Ala Thr Leu Met Ser Ala Asn Tyr
 225 230 235 240
 Pro Glu Gly Phe Pro Glu Asp Glu Leu Met Thr Trp Gln Phe Val Val

Al

Gly Val Phe Thr Val Thr Pro Asp Thr Lys Ser Lys Val Tyr Leu Arg
 545 550 555 560
 Thr Pro Asn Trp Asp Arg Gly Leu Pro Ser Leu Thr Ser Val Ser Trp
 565 570 575
 Asn Ile Ser Val Pro Arg Asp Gln Val Ala Cys Leu Thr Phe Phe Lys
 580 585 590
 Glu Arg Ser Gly Val Val Cys Gln Thr Gly Arg Ala Phe Met Ile Ile
 595 600 605
 Gln Glu Gln Arg Thr Arg Ala Glu Glu Ile Phe Ser Leu Asp Glu Asp
 610 615 620
 Val Leu Pro Lys Pro Ser Phe His His His Ser Phe Trp Val Asn Ile
 625 630 635 640
 Ser Asn Cys Ser Pro Thr Ser Gly Lys Gln Leu Asp Leu Leu Phe Ser
 645 650 655
 Val Thr Leu Thr Pro Arg Thr Val Asp Leu Thr Val Ile Leu Ile Ala
 660 665 670
 Ala Val Gly Gly Gly Val Leu Leu Leu Ser Ala Leu Gly Leu Ile Ile
 675 680 685
 Cys Cys Val Lys Lys Lys Lys Lys Lys Thr Asn Lys Gly Pro Ala Val
 690 695 700
 Gly Ile Tyr Asn Gly Asn Ile Asn Thr Glu Met Pro Arg Gln Pro Lys
 705 710 715 720
 Lys Phe Gln Lys Gly Arg Lys Asp Asn Asp Ser His Val Tyr Ala Val
 725 730 735
 Ile Glu Asp Thr Met Val Tyr Gly His Leu Leu Gln Asp Ser Ser Gly
 740 745 750
 Ser Phe Leu Gln Pro Glu Val Asp Thr Tyr Arg Pro Phe Gln Gly Thr
 755 760 765
 Met Gly Val Cys Pro Pro Ser Pro Pro Thr Ile Cys Ser Arg Ala Pro
 770 775 780
 Thr Ala Lys Leu Ala Thr Glu Glu Pro Pro Pro Arg Ser Pro Pro Glu
 785 790 795 800
 Ser Glu Ser Glu Pro Tyr Thr Phe Ser His Pro Asn Asn Gly Asp Val
 805 810 815
 Ser Ser Lys Asp Thr Asp Ile Pro Leu Leu Asn Thr Gln Glu Pro Met
 820 825 830
 Glu Pro Ala Glu
 835

<210> 5
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 5
accgcctcaa cttgttcaca tgg

23

<210> 6
<211> 26
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 6
ctggtctcag gagccagcaa cttgtc

26

<210> 7
<211> 25
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 7
ctcatgacgt ggcagtttgt cgttc

25

<210> 8
<211> 26
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 8
ggctcgtcctca ttactcaagt caacca

26

<210> 9

<211> 36
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 9
 attcgcgact gatgatcgat tttttttttt tttttt

36

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 10
 attcgcgact gatgatcgat

20

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 11
 gagatattag aattctactc

20

<210> 12
 <211> 17
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 12
 gagtagaatt ctaatat

17

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>

AI

<223> Description of the artificial sequence: Primer

<400> 13

agtccatgtg aacaagttga gg

22

<210> 14

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 14

aattctccca cctcagcctc

20

<210> 15

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 15

aggatgaaaa cgacaatgtg cc

22

<210> 16

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 16

agaattgctt gagcccagga g

21

<210> 17

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 17

caacttcaca ttgctcagtg g

21

A1

<210> 18
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 18
 tgagcaagtt cagcctgggtt aagtc

25

<210> 19
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 19
 caccgaatac tcataaagaa ggtccc

26

<210> 20
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 20
 tagacttcga gcaggagatg gccact

26

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 21
 ccagccatgt acgtagccat

20

<210> 22
 <211> 19
 <212> DNA
 <213> Artificial sequence

A1

<220>

<223> Description of the artificial sequence: Primer

<400> 22

ccaagaagga aggctggaa

19

<210> 23

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 23

ccatcacat cttccaggag cgaga

25

<210> 24

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 24

ccaagaagga aggctggaa

19

<210> 25

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 25

tgcaggaggc attgctgatg

20

<210> 26

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 26

AI

aaatcgtgca cttgcaggc

19

<210> 27
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer

<400> 27
 ttgatgcgtt ccagctga

18

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer

<400> 28
 ttgaattcac tgtgtggagc c

21

<210> 29
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer

<400> 29
 tgcaggcaac agtgatgtc

19

<210> 30
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: Primer

<400> 30
 attggccttc cttaggctgg ctac

24

<210> 31
 <211> 43

<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 31

tgtagcgtga agacgacaga aagggcgtgg taccgagctc gag

43

<210> 32

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 32

agggcgtggt accgagctcg ag

22

<210> 33

<211> 11

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 33

ggctcgagct c

11

<210> 34

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

<400> 34

ggccatgtcc ggtgggcttg tg

22

<210> 35

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer

A1

<400> 35
ctcaaaactc ctggacaagt tgctgg 26

<210> 36
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

<400> 36
aaggtgaagg tcggagtcaa cg 22

<210> 37
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

<400> 37
ggcagagatg atgacccttt tggc' 24

<210> 38
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

<400> 38
agcagcagaa cccctagcag tgc 23

<210> 39
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

<400> 39
agaacccta gcagtgcgat agagac 26

<210> 40

<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer

<400> 40
gaactgtaat gttgctttct cgtggca

A1
Conclude